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OW protein - protein search, using SW model

Run on: August 11, 2005, 08:19:50 / Search time 59 Seconds  
(without alignments)  
1145.669 Million cell updates/sec

Title: US-10-643-836-297

Perfect score: 703  
Sequence: 1 MEGAYAGAGKAGAFDPYTL.....GEPHACTPCTESTEGCPGP 132

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 50 summaries

Database: 1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	577	82.1	234 1	SNGL_HUMAN
2	550	78.2	234 1	SNGL_MOUSE
3	547	77.8	234 1	SNGL_RAT
4	500	71.1	231 2	QBRW67
5	362	51.5	229 1	SNGL_MOUSE
6	353	50.2	229 1	SNGL_HUMAN
7	306	43.5	219 2	Q6DIE7
8	304	43.2	217 2	Q6AZR4
9	296	42.1	224 1	SNGL_HUMAN
10	289.5	41.2	294 2	Q7QHR6
11	287	40.8	145 2	Q96L30
12	286	40.7	241 1	Q9V6U3
13	282	40.1	234 1	SNGL_MOUSE
14	274	39.0	224 1	SNGL_MOUSE
15	274	39.0	224 1	Q8C2Z5
16	274	39.0	224 2	Q9XK83
17	274	39.0	224 2	Q9XK83
18	211	30.0	191 2	Q6S8S7
19	192	27.3	247 1	SNGL_MOUSE
20	170	24.2	233 1	SNGL_MOUSE
21	169	24.0	234 1	SNGL_HUMAN
22	167.5	23.8	236 2	Q6R8S8
23	85	12.1	626 2	Q6R8S8
24	84.5	12.0	235 2	Q6R8S8
25	82.5	11.7	202 2	Q6R8S8
26	82	11.7	462 2	Q6R8S8
27	81.5	11.6	907 2	Q6R8S8
28	80	11.4	161 2	Q6R8S8
29	79.5	11.3	468 1	PTM8_BACHD
30	78	11.1	538 2	Q6R8S8
31	77.5	11.0	650 2	Q6R8S8

32	76	10.8	251	2	Q7ZWV8	Q7ZWV8 xenopus lae
33	76	10.8	298	2	Q6ZM74	Q6ZM74 brachydanio
34	76	10.8	439	2	Q7J1U4	Q7J1U4 bacillus ce
35	76	10.8	519	2	Q7NFM8	Q7NFM8 glieobacter
36	75.5	10.7	232	2	Q6TIG1	Q6TIG1 brachydanio
37	75.5	10.7	348	1	Y479_MYCTU	Y479_MYCTU mycobacteri
38	75.5	10.7	348	1	Y489_MYCBO	Y489_MYCBO mycobacteri
39	75.5	10.7	460	1	Q6P2F0	Q6P2F0 homo sapien
40	75.5	10.7	530	1	MATP_HUMAN	MATP_HUMAN homo sapien
41	75	10.7	249	2	Q946T4	Q946T4 oryza sativ
42	75	10.7	249	2	Q7G6Z4	Q7G6Z4 oryza sativ
43	75	10.7	439	2	Q635H8	Q635H8 bacillus ce
44	75	10.7	439	2	Q818Y3	Q818Y3 bacillus ce
45	75	10.7	439	2	Q81MC4	Q81MC4 bacillus ce
46	75	10.7	439	2	Q6HE62	Q6HE62 bacillus th
47	75	10.7	667	2	Q8VDH1	Q8VDH1 streptococc
48	75	10.7	760	2	Q6BLQ5	Q6BLQ5 debaryomyce
49	74.5	10.6	533	2	Q73FP3	Q73FP3 bacillus ce
50	74.5	10.6	533	2	Q81VY5	Q81VY5 bacillus an

## ALIGNMENTS

RESULT 1  
ID SNGL\_HUMAN STANDARD: PRT: 234 AA.  
AC 043759; 043757; 043758; 096J56; 09UG24;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Synaptoctylin-1.  
GN Name=SYNGR1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_Taxid=9606;  
RN [1]  
RP MEDLINE=98430994; PubMed=9760194;  
RA Kedar D., Pan H.-O., Seroussi B., Fransson I., Guilbaud C.,  
RA Colline J.E., Dunham I., Blennow E., Roe B.A., Piehl P.,  
RA Dumaneki J.P.,  
RA "Characterization of the human synaptoctylin gene family."  
Hum. Genet. 103:131-141(1998).  
[2]  
RP MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;  
RA Dunham I., Hunt A.R., Collins J.E., Bruskiewicz R., Beare D.M.,  
RA Clamp M., Smith L.J., Ainscough R., Almeida J.P., Babbage A.K.,  
RA Baggeley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,  
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,  
RA Burrell W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,  
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,  
RA Conroy D., Corby N.R., Corvill G.J., Cox A.V., Davis J., Dawson B.,  
RA Dham P.D., Dockree C., Dogworth S.J., Durbin R.M., Ellington A.G.,  
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,  
RA Gilbert J.G.R., Goward M.E., Graham D.V., Griffiths M.N.D., Hall C.,  
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,  
RA Hunt S.E., Jones M.C., Kerhaw J., Kimberley A.M., King A.,  
RA Laird G.K., Langford C.P., Leverish M.A., Lloyd C., Lloyd D.M.,  
RA Martin I.D., Mathergh-Mohamed M., Matthews L.H., Mccann O.T.,  
RA Mcclay C.N., McLaren S., McMurtry A.A., Milne S.A., Mortimore B.J.,  
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,  
RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L.,  
RA Scott C.B., Sehra H.K., Skuse C.D., Smalley S., Smith M.L.,  
RA Soderlund C., Spragon I., Steward C.A., Sulston J.E., Swann R.M.,  
RA Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L.,  
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,  
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,  
RA Winton S., Kawasaki K., Sasaki T., Asakawa S., Kudo N.,  
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyma S.,  
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,

RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,  
 RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,  
 RA Phan S., Qi S., Qian Y., Ray L., Ren O., Shauli S., Sloan D., Song L.,  
 RA Phan S., Qi S., Qian Y., Ray L., Ren O., Shauli S., Sloan D., Song L.,  
 RA Zhan M., Zhang G., Chiesse S., Murray J., Miller N., Mink P.,  
 RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,  
 RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,  
 RA Hinde K., Kemp K., Latreille P., Layman D., Ozeraky P., Rohlfing T.,  
 RA Scheet P., Walker C., Wamaley A., Wohldmann P., Pepin K., Nelson J.,  
 RA Korf I., Bedell J.A., Hillier L.W., Maridis E., Macreton R.,  
 RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Salita S.,  
 RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,  
 RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dunamski J.P.,  
 RA Feyerd M., Kedra D., Serousi E., Franson I., Tapia I., Bruder C.E.,  
 RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,  
 RA Khan A.S., Lane L., Tillehun Y., Wright H.,  
 RT "The DNA sequence of human chromosome 22."  
 Nature 402:489-495(1999).  
 RN  
 RP SEQUENCE FROM N.A. (ISOFORM 1B).  
 RC  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Klausner R.D., Collins F.S., Wagner L., Shamen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,  
 RA Brownstein M.J., Udén T.B., Tohbiyuki S., Carrincci P., Prange C.J.,  
 RA Rana S.S., Loguallano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wooley K.C., Hale S., Garcia A.M., Gay L.J., Huliyk S.W.,  
 RA Villalón D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Pahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M.,  
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska T., Smalins D.E.,  
 RA Scherch A., Schein J.B., Jones S.J.M., Marra M.A.,  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1A;  
 CC IsoId=O43759-1; Sequence=Displayed;  
 CC Name=1B;  
 CC IsoId=O43759-2; Sequence=VSP\_006332;  
 CC Name=1C;  
 CC IsoId=O43759-3; Sequence=VSP\_006331; VSP\_006332;  
 CC -1- SIMILARITY: Belongs to the synaptocystin family.  
 CC  
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DR Pfam, Pf01284; MARVEL, 1.  
 KW Alternative splicing; Synapse; Transmembrane.  
 FT TRANSMEM 24 44 Potential.  
 FT TRANSMEM 72 92 Potential.  
 FT TRANSMEM 104 124 Potential.  
 FT TRANSMEM 149 169 Potential.  
 FT VARSPLIC 1 33  
 FT VARSPLIC 162 234  
 FT VARSPLIC 203 203  
 FT CONFLICT 203 203 Missing (in Ref. 2).  
 FT SEQUENCE 234 AA; 25570 MW; 8B015CBBD461E12 CRC64;  
 SQ  
 Query Match 82.1%; Score 577; DB 1; Length 234;  
 Best Local Similarity 99.1%; Pred. No. 1.7e-46;  
 Matches 111; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MEGAYAGKAGKAGAFDPYTLVROPHITLRVYSMTFSIVFGSIVNKGYSASBEGQFCI 60  
 DB 1 MEGAYAGKAGKAGAFDPYTLVROPHITLRVYSMTFSIVFGSIVNKGYSASBEGQFCI 60  
 QY 61 YNRPNMNCYSVAVGVLAFLTCLLYALDVFYPOISSVDRKRAVLSDIGVS 112  
 DB 61 YNRPNMNCYSVAVGVLAFLTCLLYALDVFYPOISSVDRKRAVLSDIGVS 112  
 RESULT 2  
 ID SNG1\_MOUSE STANDARD; PRT; 234 AA.  
 AC 055100; O9DCB0;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Synaptocystin-1.  
 GN Name=Syngr1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RP SEQUENCE FROM N.A. (ISOFORM 1B).  
 RX MEDLINE=98430994; PubMed=9760194;  
 RA Kedra D., Pan H.-Q., Serousi E., Franson I., Guilbaud C.,  
 RA Collins U.E., Dunham I., Blennow E., Roe B.A., Piehl F.,  
 RA Dunneki J.P.,  
 RT "Characterization of the human synaptocystin gene family."  
 RL Hum. Genet. 103:131-141(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1A AND 1B).  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Nishida I., Otsu N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Balcells J., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schmitt L.M., Kanapin A., Matsumura H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Brad D., Brusic V., Chochla C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forster K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,  
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Kongweya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Nunata K., Okido T., Pavan W.J., Petrea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sempke C.A., Seroussi E., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomlita M.,

RA Varado R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carrinci P., Hayatsu N.,  
 RA Hirozane-Klehlkawa T., Kono H., Nakamura M., Sakakura N., Sato K.,  
 RA Shiraki T., Waki K., Kawel J., Aizawa K., Aikawa T., Fukuda S.,  
 RA Hara A., Haseizume M., Imocani D., Shibata K., Shingawa A.,  
 RA Miyazaki A., Sakai K., Ishii Y., Itoh M., Kagawa I.,  
 RA Yasumehi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.,  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs."  
 RL Nature 420:563-573 (2002).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=1A;  
 CC IsoId=O55100-1; Sequence=Displayed;  
 CC Name=1B;  
 CC IsoId=O55100-2; Sequence=VSP\_006333;  
 CC -1- SIMILARITY: Belongs to the synaptogyrin family.  
 CC -----  
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 CC -----  
 CC EMBL: AJ002306; CA05323.1; -  
 DR EMBL: AK002972; BAB22487.1; -  
 DR EMBL: AK010442; BAB26943.1; -  
 DR MGI: MGI:1328323; Syngri.  
 DR InterPro: IPR008253; Marvel.  
 DR Pfam: PF01284; MARVEL; 1.  
 DR Alternative splicing; Synapse; Transmembrane.  
 FT TRANSMEM 24 44 Potential.  
 FT TRANSMEM 72 92 Potential.  
 FT TRANSMEM 104 124 Potential.  
 FT TRANSMEM 149 169 Potential.  
 FT VASPLC 162 234 Potential.  
 FT AGQAVLAFGRYQIGADSLFSDQDYNPSQSSMPYAPYEP  
 FT SAGSDPAGNGGYOHFANPADEAPQGYQGY -> SLTAA  
 FT LAVRRPKELTFOEYVTLFPASAP (in isoform  
 1B).  
 FT FTId=VSP\_006333.  
 FT SEQUENCE 234 AA; 25653 MW; 0956602IDP3E809A CRC64;  
 SO  
 Query Match 78.2%; Score 550; DB 1; Length 234;  
 Best Local Similarity 93.8%; Pred. No. 6.1e-44;  
 Matches 105; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 MEGAYGAGKAGAPDPTLVROPHITLVSVLSIVVFGSIVNMGYLSASBEGQFCI 60  
 DB 1 MEGAYGAGKAGAPDPTLVROPHITLVSVLSIVVFGSIVNMGYLSANPEEBEFCI 60  
 QY 61 YNRNPACGYGAVGLAFITCLLYTALDVYFPQISSVDRKKAVALSDIGVS 112  
 DB 61 YNRNPACGYGAVGLAFITCLLYTALDVYFPQISSVDRKKAVALSDIGVS 112  
 RESULT 3  
 SNG1\_RAT STANDARD; PRT; 234 AA.  
 AC Q62876;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Synaptogyrin-1 (p29).  
 GN Name=Syngri;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=96134029; PubMed=8557746; DOI=10.1063/jcb.131.6.1801;  
 RX Stenius K., Jantz R., Suedhof T.C., Jahn R.;  
 RT "Structure of synaptogyrin (p29) defines novel synaptic vesicle  
 protein."  
 RL Cell Biol. 131:1801-1809 (1995).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- TISSUE SPECIFICITY: Nervous system.  
 CC -1- SIMILARITY: Belongs to the synaptogyrin family.  
 CC -----  
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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 CC EMBL: U39549; AAB17890.1; -  
 DR RGD; 3801; Syngri.  
 DR InterPro: IPR008253; Marvel.  
 DR Pfam: PF01284; MARVEL; 1.  
 DR Synapse; Transmembrane.  
 FT TRANSMEM 24 44 Potential.  
 FT TRANSMEM 72 92 Potential.  
 FT TRANSMEM 105 125 Potential.  
 FT TRANSMEM 149 169 Potential.  
 SO SEQUENCE 234 AA; 25669 MW; B303864C49F31E1 CRC64;  
 QY 1 MEGAYGAGKAGAPDPTLVROPHITLVSVLSIVVFGSIVNMGYLSASBEGQFCI 60  
 DB 1 MEGAYGAGKAGAPDPTLVROPHITLVSVLSIVVFGSIVNMGYLSANPEEBEFCI 60  
 QY 61 YNRNPACGYGAVGLAFITCLLYTALDVYFPQISSVDRKKAVALSDIGVS 112  
 DB 61 YNRNPACGYGAVGLAFITCLLYTALDVYFPQISSVDRKKAVALSDIGVS 112  
 RESULT 4  
 Q8UM67 PRELIMINARY; PRT; 231 AA.  
 ID Q8UM67;  
 AC Q8UM67;  
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE P7D11.  
 GN Name=P7D11;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21643879; PubMed=11784032; DOI=10.1006/dbio.2001.0428;  
 RA Shibata M., Itoh M., Ohmori S., Shinga J., Taira M.;  
 RT "Systematic screening and expression analysis of the head organizer  
 genes in Xenopus embryos."  
 RL Dev. Biol. 239:241-256 (2001).  
 DR EMBL: AB072005; BAB79596.1; -  
 DR GO: GO:0016020; C:membrane; IEA.  
 DR Pfam: PF01284; MARVEL; 1.  
 SO SEQUENCE 231 AA; 25535 MW; 03962F903EBE3F14 CRC64;  
 QY 1 MEGAYGAGKAGAPDPTLVROPHITLVSVLSIVVFGSIVNMGYLSASBEGQFCI 60  
 DB 1 MEGAYGAGKAGAPDPTLVROPHITLVSVLSIVVFGSIVNMGYLSANPEEBEFCI 60  
 QY 61 YNRNPACGYGAVGLAFITCLLYTALDVYFPQISSVDRKKAVALSDIGVS 112  
 DB 61 YNRNPACGYGAVGLAFITCLLYTALDVYFPQISSVDRKKAVALSDIGVS 112  
 Query Match 71.1%; Score 500; DB 2; Length 231;  
 Best Local Similarity 81.2%; Pred. No. 3.3e-39;  
 Matches 91; Conservative 13; Mismatches 8; Indels 0; Gaps 0;